RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/849,868**

DATE: 06/05/2001
TIME: 13:11:28

Input Set : **A:\seqlist.txt**
Output Set: **C:\CRF3\06052001\I849868.raw**

ENTERED

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  4 <110> APPLICANT: Genentech, Inc.
  5         Gao, Wei-Qiang
  7 <120> TITLE OF INVENTION: HAIR CELL DISORDERS
 10 <130> FILE REFERENCE: GENENT.035VPC
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/849,868
C--> 12 <141> CURRENT FILING DATE: 2001-05-04
 12 <160> NUMBER OF SEQ ID NOS: 14
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 669
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
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 23  1               5                  10                  15
.24 Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro Ala Pro
 25              20                  25                  30
 26 Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met Ser Glu Arg
 27              35                  40·                 45
 28 Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser
 29      50                  55                  60
 30 Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
 31 65                  70                  75                  80
 32 Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys
 33              85                  90                  95
 34 Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe
 35              100                 105                 110
 36 Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln
 37              115                 120                 125
 38 Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn
 39      130                 135                 140
 40 Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser
 41 145                 150                 155                 160
 42 Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser
 43              165                 170                 175
 44 Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val
 45              180                 185                 190
 46 Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn
 47              195                 200                 205
 48 Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
 49      210                 215                 220
 50 Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 51 225                 230                 235                 240
 52 Phe Met Val Lys. Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
 53              245                 250                 255
 54 Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 55              260                 265                 270
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 56 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu
 57         275             280                 285
 58 Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
 59     290             295                 300
 60 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp
 61 305             310                 315                 320
 62 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile
 63             325                 330                 335
 64 Ala Asn Gly Pro His His Pro Asn Pro Pro Glu Asn Val Gln Leu
 65             340                 345                 350
 66 Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val
 67         355                 360                 365
 68 Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr
 69     370             375                 380
 70 Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser
 71 385             390                 395                 400
 72 Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile Val
 73             405                 410                 415
 74 Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro
 75         420                 425                 430
 76 Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe
 77         435                 440                 445
 78 Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His
 79     450             455                 460
 80 Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
 81 465             470                 475                 480
 82 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met
 83             485                 490                 495
 84 Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala Val
 85         500                 505                 510
 86 Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro
 87         515                 520                 525
 88 Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser
 89     530                 535                 540
 90 Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro
 91 545                 550                 555                 560
 92 Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu
 93             565                 570                 575
 94 Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys
 95         580                 585                 590
 96 Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser
 97         595                 600                 605
 98 Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu
 99     610                 615                 620
100 Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala
101 625                 630                 635                 640
102 Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr
103                 645                 650                 655
104 Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln
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105          660              665
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 2226
110 <212> TYPE: DNA
111 <213> ORGANISM: Homo sapiens
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (2)...(2008)
117 <400> SEQUENCE: 2
118 g ggc gcg agc gcc tca gcg cgg ccg ctc gct ctc ccc ctc gag gga caa 49
119   Gly Ala Ser Ala Ser Ala Arg Pro Leu Ala Leu Pro Leu Glu Gly Gln
120   1               5                   10                  15
122 act ttt ccc aaa ccc gat ccg agc cct tgg acc aaa ctc gcc tgc gcc   97
123 Thr Phe Pro Lys Pro Asp Pro Ser Pro Trp Thr Lys Leu Ala Cys Ala
124             20                  25                  30
126 gag agc cgt ccg cgt aga gcg ctc cgt ctc cgg cga gat gtc cga gcg  145
127 Glu Ser Arg Pro Arg Arg Ala Leu Arg Leu Arg Arg Asp Val Arg Ala
128         35                  40                  45
130 caa aga agg cag agg caa agg gaa ggg caa gaa gaa gga gcg agg ctc  193
131 Gln Arg Arg Gln Arg Gln Arg Glu Gly Gln Glu Glu Gly Ala Arg Leu
132     50                  55                  60
134 cgg caa gaa gcc gga gtc cgc ggc ggg cag cca gag ccc agc ctt gcc  241
135 Arg Gln Glu Ala Gly Val Arg Gly Gly Gln Pro Glu Pro Ser Leu Ala
136 65                  70                  75                  80
138 tcc ccg att gaa aga gat gaa aag cca gga atc ggc tgc agg ttc caa  289
139 Ser Pro Ile Glu Arg Asp Glu Lys Pro Gly Ile Gly Cys Arg Phe Gln
140             85                  90                  95
142 act agt cct tcg gtg tga aac cag ttc tga ata ctc ctc tct cag att  337
143 Thr Ser Pro Ser Val  *  Asn Gln Phe  *  Ile Leu Leu Ser Gln Ile
144             100                 105                 110
146 caa gtg gtt caa gaa tgg gaa tga att gaa tcg aaa aaa caa acc aca  385
147 Gln Val Val Gln Glu Trp Glu  *  Ile Glu Ser Lys Lys Gln Thr Thr
148             115                 120                 125
150 aaa tat caa gat aca aaa aaa gcc agg gaa gtc aga act tcg cat taa  433
151 Lys Tyr Gln Asp Thr Lys Lys Ala Arg Glu Val Arg Thr Ser His  *
152             130                 135                 140
154 caa agc atc act ggc tga ttc tgg aga gta tat gtg caa agt gat cag  481
155 Gln Ser Ile Thr Gly  *  Phe Trp Arg Val Tyr Val Gln Ser Asp Gln
156             145                 150                 155
158 caa att agg aaa tga cag tgc ctc tgc caa tat cac cat cgt gga atc  529
159 Gln Ile Arg Lys  *  Gln Cys Leu Cys Gln Tyr His His Arg Gly Ile
160             160                 165                 170
162 aaa cga gat cat cac tgg tat gcc agc ctc aac tga agg agc ata tgt  577
163 Lys Arg Asp His His Trp Tyr Ala Ser Leu Asn  *  Arg Ser Ile Cys
164             175                 180                 185
166 gtc ttc aga gtc tcc cat tag aat atc agt atc cac aga agg agc aaa  625
167 Val Phe Arg Val Ser His  *  Asn Ile Ser Ile His Arg Arg Ser Lys
168             190                 195                 200
170 tac ttc ttc atc tac atc tac atc cac cac tgg gac aag cca tct tgt  673
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171 Tyr Phe Phe Ile Tyr Ile Tyr Ile His His Trp Asp Lys Pro Ser Cys
172             205             210             215
174 aaa atg tgc gga gaa gga gaa aac ttt ctg tgt gaa tgg agg gga gtg     721
175 Lys Met Cys Gly Glu Gly Glu Asn Phe Leu Cys Glu Trp Arg Gly Val
176             220             225             230
178 ctt cat ggt gaa aga cct ttc aaa ccc ctc gag ata ctt gtg caa gtg     769
179 Leu His Gly Glu Arg Pro Phe Lys Pro Leu Glu Ile Leu Val Gln Val
180             235             240             245
182 cca acc tgg att cac tgg agc aag atg tac tga gaa tgt gcc cat gaa     817
183 Pro Thr Trp Ile His Trp Ser Lys Met Tyr  *  Glu Cys Ala His Glu
184             250             255             260
186 agt cca aaa cca aga aaa ggc gga gga gct gta cca gaa gag agt gct     865
187 Ser Pro Lys Pro Arg Lys Gly Gly Gly Ala Val Pro Glu Glu Ser Ala
188             265             270             275
190 gac cat aac cgg cat ctg cat cgc cct cct tgt ggt cgg cat cat gtg     913
191 Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val
192 280             285             290             295
194 tgt ggt ggc cta ctg caa aac caa gaa aca gcg gaa aaa gct gca tga     961
195 Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala  *
196             300             305             310
198 ccg tct tcg gca gag cct tcg gtc tga acg aaa caa tat gat gaa cat    1009
199 Pro Ser Ser Ala Glu Pro Ser Val  *  Thr Lys Gln Tyr Asp Glu His
200             315             320             325
202 tgc caa tgg gcc tca cca tcc taa ccc acc ccc cga gaa tgt cca gct    1057
203 Cys Gln Trp Ala Ser Pro Ser  *  Pro Thr Pro Arg Glu Cys Pro Ala
204             330             335             340
206 ggt gaa tca ata cgt atc taa aaa cgt cat ctc cag tga gca tat tgt    1105
207 Gly Glu Ser Ile Arg Ile  *  Lys Arg His Leu Gln  *  Ala Tyr Cys
208             345             350
210 tga gag aga agc aga gac atc ctt ttc cac cag tca cta tac ttc cac    1153
211  *  Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu Tyr Phe His
212     355             360             365
214 agc cca tca ctc cac tac tgt cac cca gac tcc tag cca cag ctg gag    1201
215 Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser  *  Pro Gln Leu Glu
216 370             375             380
218 caa cgg aca cac tga aag cat cct ttc cga aag cca ctc tgt aat cgt    1249
219 Gln Arg Thr His  *  Lys His Pro Phe Arg Lys Pro Leu Cys Asn Arg
220 385             390             395
222 gat gtc atc cgt aga aaa cag tag gca cag cag ccc aac tgg ggg ccc    1297
223 Asp Val Ile Arg Arg Lys Gln  *  Ala Gln Gln Pro Asn Trp Gly Pro
224 400             405             410
226 aag agg acg tct taa tgg cac agg agg ccc tcg tga atg taa cag ctt    1345
227 Lys Arg Thr Ser  *  Trp His Arg Arg Pro Ser  *  Met  *  Gln Leu
228 415             420             425
230 cct cag gca tgc cag aga aac ccc tga ttc cta ccg aga ctc tcc tca    1393
231 Pro Gln Ala Cys Gln Arg Asn Pro  *  Phe Leu Pro Arg Leu Ser Ser
232             430             435             440
234 tag tga aag gta tgt gtc agc cat gac cac ccc ggc tcg tat gtc acc    1441
235  *   *  Lys Val Cys Val Ser His Asp His Pro Gly Ser Tyr Val Thr
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236                 445              450              455
238 tgt aga ttt cca cac gcc aag ctc ccc caa atc gcc ccc ttc gga aat   1489
239 Cys Arg Phe Pro His Ala Lys Leu Pro Gln Ile Ala Pro Phe Gly Asn
240             460              465              470
242 gtc tcc acc cgt gtc cag cat gac ggt gtc cat gcc ttc cat ggc ggt   1537
243 Val Ser Thr Arg Val Gln His Asp Gly Val His Ala Phe His Gly Gly
244             475              480              485
246 cag ccc ctt cat gga aga aga gag acc tct act tct cgt gac acc acc   1585
247 Gln Pro Leu His Gly Arg Arg Glu Thr Ser Thr Ser Arg Asp Thr Thr
248     490              495              500
250 aag gct gcg gga gaa gaa gtt tga cca tca ccc tca gca gtt cag ctc   1633
251 Lys Ala Ala Gly Glu Glu Val  *  Pro Ser Pro Ser Ala Val Gln Leu
252 505             510              515
254 ctt cca cca caa ccc cgc gca tga cag taa cag cct ccc tgc tag ccc   1681
255 Leu Pro Pro Gln Pro Arg Ala  *  Gln  *  Gln Pro Pro Cys  *  Pro
256 520             525              530
258 ctt gag gat agt gga gga tga gga gta tga aac gac cca aga gta cga   1729
259 Leu Glu Asp Ser Gly Gly  *  Gly Val  *  Asn Asp Pro Arg Val Arg
260             535              540              545
262 gcc agc cca aga gcc tgt taa gaa act cgc caa tag ccg gcg ggc caa   1777
263 Ala Ser Pro Arg Ala Cys  *  Glu Thr Arg Gln  *  Pro Ala Gly Gln
264             550              555              560
266 aag aac caa gcc caa tgg cca cat tgc taa cag att gga agt gga cag   1825
267 Lys Asn Gln Ala Gln Trp Pro His Cys  *  Gln Ile Gly Ser Gly Gln
268             565              570              575
270 caa cac aag ctc cca gag cag taa ctc aga gag tga aac aga aga tga   1873
271 Gln His Lys Leu Pro Glu Gln  *  Leu Arg Glu  *  Asn Arg Arg  *
272             580              585
274 aag agt agg tga aga tac gcc ttt cct ggg cat aca gaa ccc cct ggc   1921
275 Lys Ser Arg  *  Arg Tyr Ala Phe Pro Gly His Thr Glu Pro Pro Gly
276     590              595              600
278 agc cag tct tga ggc aac acc tgc ctt ccg cct ggc tga cag cag gac   1969
279 Ser Gln Ser  *  Gly Asn Thr Cys Leu Pro Pro Gly  *  Gln Gln Asp
280     605              610              615
282 taa ccc agc agg ccg ctt ctc gac aca gga aga aat cca ggccaggctg   2018
283  *  Pro Ser Arg Pro Leu Leu Asp Thr Gly Arg Asn Pro
284             620              625
286 tctagtgtaa ttgctaacca agaccctatt gctgtataaa acctaaataa acacatagat 2078
287 tcacctgtaa aactttattt tatataataa agtattccac cttaaattaa acaatttatt 2138
288 ttattttagc agttctgcaa atagaaaaca ggaaaaaaac ttttataaat taaatatatg 2198
289 tatgtaaaaa tgaaaaaaaa aaaaaaaa                                     2226
291 <210> SEQ ID NO: 3
292 <211> LENGTH: 675
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <400> SEQUENCE: 3
297 Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro
298 1               5                10               15
299 Ala Pro Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met Ser
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VERIFICATION SUMMARY   DATE: 06/05/2001
PATENT APPLICATION: **US/09/849,868**   TIME: 13:11:29

Input Set : **A:\seqlist.txt**
Output Set: **C:\CRF3\06052001\I849868.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date